SEQUENCE LISTING

<110> Fibrogen, Inc.
Grotendorst, Gary
Neff, Thomas

10550

<120> Connective Tissue Growth Factor Fragments and Methods and Uses Thereof

<130> FIBRO1130-2

<140> 09/461,646
<141> 1999-12-14

<150> 60/112,240
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<170> PatentIn version 3.0

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gtgccaacc atg acc gcc gcc agt atg ggc ccc gtc cgc gtc gcc ttc gtg    171
          Met Thr Ala Ala Ser Met Gly Pro Val Arg Val Ala Phe Val
          1               5                  10

gtc ctc ctc gcc ctc tgc agc cgg ccg gcc gtc ggc cag aac tgc agc      219
Val Leu Leu Ala Leu Cys Ser Arg Pro Ala Val Gly Gln Asn Cys Ser
15                  20                  25                  30

ggg ccg tgc cgg tgc ccg gac gag ccg gcg ccg cgc tgc ccg gcg ggc      267
Gly Pro Cys Arg Cys Pro Asp Glu Pro Ala Pro Arg Cys Pro Ala Gly
                35                  40                  45

gtg agc ctc gtg ctg gac ggc tgc ggc tgc tgc cgc gtc tgc gcc aag      315
Val Ser Leu Val Leu Asp Gly Cys Gly Cys Cys Arg Val Cys Ala Lys
            50                  55                  60

cag ctg ggc gag ctg tgc acc gag cgc gac ccc tgc gac ccg cac aag      363
Gln Leu Gly Glu Leu Cys Thr Glu Arg Asp Pro Cys Asp Pro His Lys
        65                  70                  75

ggc ctc ttc tgt gac ttc ggc tcc ccg gcc aac cgc aag atc ggc gtg      411
Gly Leu Phe Cys Asp Phe Gly Ser Pro Ala Asn Arg Lys Ile Gly Val
    80                  85                  90

tgc acc gcc aaa gat ggt gct ccc tgc atc ttc ggt ggt acg gtg tac      459
Cys Thr Ala Lys Asp Gly Ala Pro Cys Ile Phe Gly Gly Thr Val Tyr
95                  100                 105                 110
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A

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cgc agc gga gag tcc ttc cag agc agc tgc aag tac cag tgc acg tgc      507
Arg Ser Gly Glu Ser Phe Gln Ser Ser Cys Lys Tyr Gln Cys Thr Cys
                115                 120                 125

ctg gac ggg gcg gtg ggc tgc atg ccc ctg tgc agc atg gac gtt cgt      555
Leu Asp Gly Ala Val Gly Cys Met Pro Leu Cys Ser Met Asp Val Arg
            130                 135                 140

ctg ccc agc cct gac tgc ccc ttc ccg agg agg gtc aag ctg ccc ggg      603
Leu Pro Ser Pro Asp Cys Pro Phe Pro Arg Arg Val Lys Leu Pro Gly
        145                 150                 155

aaa tgc tgc gag gag tgg gtg tgt gac gag ccc aag gac caa acc gtg      651
Lys Cys Cys Glu Glu Trp Val Cys Asp Glu Pro Lys Asp Gln Thr Val
    160                 165                 170

gtt ggg cct gcc ctc gcg gct tac cga ctg gaa gac acg ttt ggc cca      699
Val Gly Pro Ala Leu Ala Ala Tyr Arg Leu Glu Asp Thr Phe Gly Pro
175                 180                 185                 190

gac cca act atg att aga gcc aac tgc ctg gtc cag acc aca gag tgg      747
Asp Pro Thr Met Ile Arg Ala Asn Cys Leu Val Gln Thr Thr Glu Trp
                195                 200                 205

agc gcc tgt tcc aag acc tgt ggg atg ggc atc tcc acc cgg gtt acc      795
Ser Ala Cys Ser Lys Thr Cys Gly Met Gly Ile Ser Thr Arg Val Thr
            210                 215                 220

aat gac aac gcc tcc tgc agg cta gag aag cag agc cgc ctg tgc atg      843
Asn Asp Asn Ala Ser Cys Arg Leu Glu Lys Gln Ser Arg Leu Cys Met
        225                 230                 235

gtc agg cct tgc gaa gct gac ctg gaa gag aac att aag aag ggc aaa      891
Val Arg Pro Cys Glu Ala Asp Leu Glu Glu Asn Ile Lys Lys Gly Lys
    240                 245                 250

aag tgc atc cgt act ccc aaa atc tcc aag cct atc aag ttt gag ctt      939
Lys Cys Ile Arg Thr Pro Lys Ile Ser Lys Pro Ile Lys Phe Glu Leu
255                 260                 265                 270

tct ggc tgc acc agc atg aag aca tac cga gct aaa ttc tgt gga gta      987
Ser Gly Cys Thr Ser Met Lys Thr Tyr Arg Ala Lys Phe Cys Gly Val
                275                 280                 285

tgt acc gac ggc cga tgc tgc acc ccc cac aga acc acc acc ctg ccg     1035
Cys Thr Asp Gly Arg Cys Cys Thr Pro His Arg Thr Thr Thr Leu Pro
            290                 295                 300

gtg gag ttc aag tgc cct gac ggc gag gtc atg aag aag aac atg atg     1083
Val Glu Phe Lys Cys Pro Asp Gly Glu Val Met Lys Lys Asn Met Met
        305                 310                 315

ttc atc aag acc tgt gcc tgc cat tac aac tgt ccc gga gac aat gac     1131
Phe Ile Lys Thr Cys Ala Cys His Tyr Asn Cys Pro Gly Asp Asn Asp
    320                 325                 330

atc ttt gaa tcg ctg tac tac agg aag atg tac gga gac atg gca         1176
Ile Phe Glu Ser Leu Tyr Tyr Arg Lys Met Tyr Gly Asp Met Ala
335                 340                 345

tgaagccaga gagtgagaga cattaactca ttagactgga acttgaactg attcacatct   1236

catttttccg taaaaatgat ttcagtagca caagttattt aaatctgttt ttctaactgg   1296

gggaaaagat tcccacccaa ttcaaaacat tgtgccatgt caaacaaata gtctatcttc   1356
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ccagaatgta tattaaggtg tggctttagg agcagtggga gggtaccggc ccggttagta 1476

tcatcagatc gactcttata cgagtaatat gcctgctatt tgaagtgtaa ttgagaagga 1536

aaatttagc gtgctcactg acctgcctgt agccccagtg acagctagga tgtgcattct 1596

ccagccatca agagactgag tcaagttgtt ccttaagtca gaacagcaga ctcagctctg 1656

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Cys Arg Cys Pro Asp Glu Pro Ala Pro Arg Cys Pro Ala Gly Val Ser
35 40 45

Leu Val Leu Asp Gly Cys Gly Cys Cys Arg Val Cys Ala Lys Gln Leu
50 55 60

Gly Glu Leu Cys Thr Glu Arg Asp Pro Cys Asp Pro His Lys Gly Leu
65 70 75 80

Phe Cys Asp Phe Gly Ser Pro Ala Asn Arg Lys Ile Gly Val Cys Thr
85 90 95

Ala Lys Asp Gly Ala Pro Cys Ile Phe Gly Gly Thr Val Tyr Arg Ser
100 105 110

Gly Glu Ser Phe Gln Ser Ser Cys Lys Tyr Gln Cys Thr Cys Leu Asp
115 120 125

a' cont

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Gly Ala Val Gly Cys Met Pro Leu Cys Ser Met Asp Val Arg Leu Pro
    130                 135                 140

Ser Pro Asp Cys Pro Phe Pro Arg Arg Val Lys Leu Pro Gly Lys Cys
145                 150                 155                 160

Cys Glu Glu Trp Val Cys Asp Glu Pro Lys Asp Gln Thr Val Val Gly
                165                 170                 175

Pro Ala Leu Ala Ala Tyr Arg Leu Glu Asp Thr Phe Gly Pro Asp Pro
            180                 185                 190

Thr Met Ile Arg Ala Asn Cys Leu Val Gln Thr Thr Glu Trp Ser Ala
        195                 200                 205

Cys Ser Lys Thr Cys Gly Met Gly Ile Ser Thr Arg Val Thr Asn Asp
    210                 215                 220

Asn Ala Ser Cys Arg Leu Glu Lys Gln Ser Arg Leu Cys Met Val Arg
225                 230                 235                 240

Pro Cys Glu Ala Asp Leu Glu Glu Asn Ile Lys Lys Gly Lys Lys Cys
                245                 250                 255

Ile Arg Thr Pro Lys Ile Ser Lys Pro Ile Lys Phe Glu Leu Ser Gly
            260                 265                 270

Cys Thr Ser Met Lys Thr Tyr Arg Ala Lys Phe Cys Gly Val Cys Thr
        275                 280                 285

Asp Gly Arg Cys Cys Thr Pro His Arg Thr Thr Thr Leu Pro Val Glu
    290                 295                 300

Phe Lys Cys Pro Asp Gly Glu Val Met Lys Lys Asn Met Met Phe Ile
305                 310                 315                 320

Lys Thr Cys Ala Cys His Tyr Asn Cys Pro Gly Asp Asn Asp Ile Phe
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Glu Ser Leu Tyr Tyr Arg Lys Met Tyr Gly Asp Met Ala
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atg att aga gcc aac tgc ctg gtc cag acc aca gag tgg agc gcc tgt       96
Met Ile Arg Ala Asn Cys Leu Val Gln Thr Thr Glu Trp Ser Ala Cys
            20                  25                  30

tcc aag acc tgt ggg atg ggc atc tcc acc cgg gtt acc aat gac aac      144
Ser Lys Thr Cys Gly Met Gly Ile Ser Thr Arg Val Thr Asn Asp Asn
        35                  40                  45

gcc tcc tgc agg cta gag aag cag agc cgc ctg tgc atg gtc agg cct      192
Ala Ser Cys Arg Leu Glu Lys Gln Ser Arg Leu Cys Met Val Arg Pro
    50                  55                  60

tgc gaa gct gac ctg gaa gag aac att aag aag ggc aaa aag tgc atc      240
Cys Glu Ala Asp Leu Glu Glu Asn Ile Lys Lys Gly Lys Lys Cys Ile
65                  70                  75                  80

cgt act ccc aaa atc tcc aag cct atc aag ttt gag ctt tct ggc tgc      288
Arg Thr Pro Lys Ile Ser Lys Pro Ile Lys Phe Glu Leu Ser Gly Cys
                85                  90                  95

acc agc atg aag aca tac cga gct aaa ttc tgt gga gta tgt acc gac      336
Thr Ser Met Lys Thr Tyr Arg Ala Lys Phe Cys Gly Val Cys Thr Asp
            100                 105                 110

ggc cga tgc tgc acc ccc cac aga acc acc acc ctg ccg gtg gag ttc      384
Gly Arg Cys Cys Thr Pro His Arg Thr Thr Thr Leu Pro Val Glu Phe
        115                 120                 125

aag tgc cct gac ggc gag gtc atg aag aag aac atg atg ttc atc aag      432
Lys Cys Pro Asp Gly Glu Val Met Lys Lys Asn Met Met Phe Ile Lys
    130                 135                 140

acc tgt gcc tgc cat tac aac tgt ccc gga gac aat gac atc ttt gaa      480
Thr Cys Ala Cys His Tyr Asn Cys Pro Gly Asp Asn Asp Ile Phe Glu
145                 150                 155                 160

tcg ctg tac tac agg aag atg tac gga gac atg gca tgaagccaga           526
Ser Leu Tyr Tyr Arg Lys Met Tyr Gly Asp Met Ala
                165                 170
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a1 Cont

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tcccacccaa ttcaaaacat tgtgccatgt caaacaaata gtctatcttc cccagacact    706

ggtttgaaga atgttaagac ttgacagtgg aactacatta gtacacagca ccagaatgta    766

tattaaggtg tggctttagg agcagtggga gggtaccggc ccggttagta tcatcagatc    826

gactcttata cgagtaatat gcctgctatt tgaagtgtaa ttgagaagga aaattttagc    886

gtgctcactg acctgcctgt agccccagtg acagctagga tgtgcattct ccagccatca    946

agagactgag tcaagttgtt ccttaagtca gaacagcaga ctcagctctg acattctgat   1006

tcgaatgaca ctgttcagga atcggaatcc tgtcgattag actggacagc ttgtggcaag   1066

tgaatttgcc tgtaacaagc cagatttttt aaaatttata ttgtaaatat tgtgtgtgtg   1126
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A

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accataggta gaatgtaaag cttgtctgat cgttcaaagc atgaaatgga tacttatatg 1306

gaaattctgc tcagatagaa tgacagtccg tcaaaacaga ttgtttgcaa aggggaggca 1366

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Ala Leu Ala Ala Tyr Arg Leu Glu Asp Thr Phe Gly Pro Asp Pro Thr
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Met Ile Arg Ala Asn Cys Leu Val Gln Thr Thr Glu Trp Ser Ala Cys
20 25 30

Ser Lys Thr Cys Gly Met Gly Ile Ser Thr Arg Val Thr Asn Asp Asn
35 40 45

Ala Ser Cys Arg Leu Glu Lys Gln Ser Arg Leu Cys Met Val Arg Pro
50 55 60

Cys Glu Ala Asp Leu Glu Glu Asn Ile Lys Lys Gly Lys Lys Cys Ile
65 70 75 80

Arg Thr Pro Lys Ile Ser Lys Pro Ile Lys Phe Glu Leu Ser Gly Cys
85 90 95

Thr Ser Met Lys Thr Tyr Arg Ala Lys Phe Cys Gly Val Cys Thr Asp
100 105 110

Gly Arg Cys Cys Thr Pro His Arg Thr Thr Thr Leu Pro Val Glu Phe
115 120 125

Lys Cys Pro Asp Gly Glu Val Met Lys Lys Asn Met Met Phe Ile Lys
130 135 140

Thr Cys Ala Cys His Tyr Asn Cys Pro Gly Asp Asn Asp Ile Phe Glu
145 150 155 160

Ser Leu Tyr Tyr Arg Lys Met Tyr Gly Asp Met Ala
165 170

a1 cont

A